

Additional file 3: Figure S1. **A.** Multiple sequence alignment of amino acid sequences was performed using MUSCLE method. BIR domains: grey boxes; RING domain: bold letters. **B.** Phylogenetic tree of tick IAPs. The tree was constructed with IAP amino acid sequences from 15 tick species (accession numbers available in Additional file 1: Table S1) using Maximum Likelihood (ML) method. Bar scale at the bottom indicates 10% amino acid divergence.

A. *Dermacentor reticulatus*

Hyalomma excavatum
Rhipicephalus pulchellus
Rhipicephalus appendiculatus
Rhipicephalus zambeziensis
Rhipicephalus microplus
Amblyomma maculatum
Amblyomma triste
Amblyomma sculptum
Amblyomma aureolatum
Ixodes ricinus
Ixodes scapularis
Ornithodoros moubata
Ornithodoros erraticus
Ornithodoros turicata

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----------------------------------------RG-----
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-----ERTVTDGLGSK-----PISMDAVNMSPD--LSQEEVRLETFNNRWPNNPPIASKLAQG
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Dermacentor reticulatus

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Ixodes scapularis
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*:***: *:**

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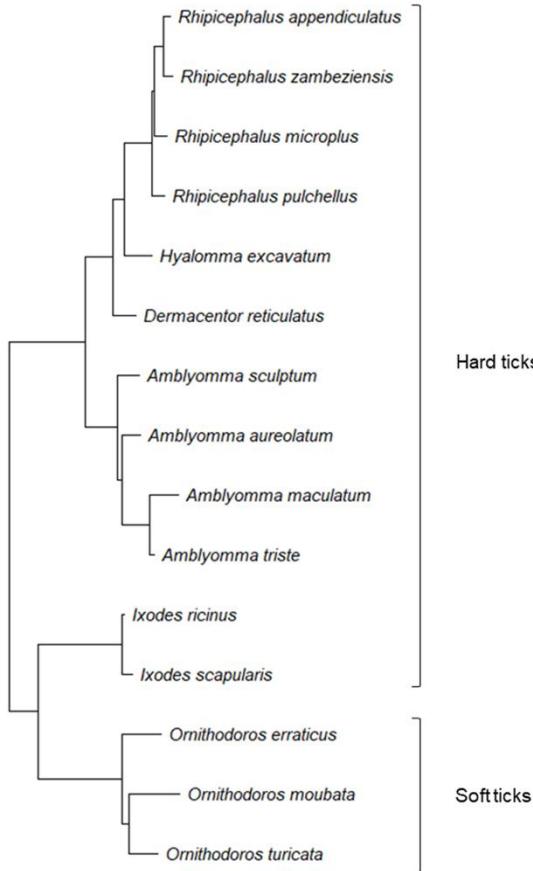
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B.



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